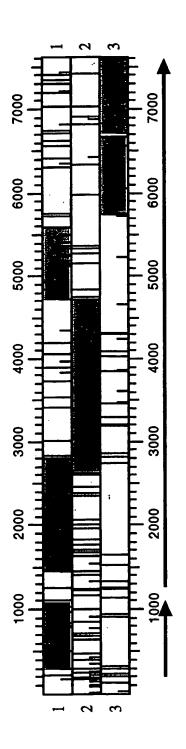
5 6 7 8 9 10 11 12 13 14 15 23,130 9,416 6,557 4,361 2,322 2,027 564 Fig. 1 pRC158 EcoRI 23130 9416 6557 4.3 3.4 2.9 2.2 2322 2027 Size Marker Fragment (Bp) Size (Kb)

Fig. 2

SUBSTITUTE SHEET (RULE 26)

Fig 3



	nitiator Codon	Initiator Codon Terminator Codon	Molecular Weight
Regulator	295		27102
Transport	1450	2805	
Monooxygenase	2810		
semialdehyde I	4717		
Catechol 2,3-dioxygenase	5721		
Alcohol dehydrogenase	1179	7580	

Fig 4

10 30 50 GAATTCCATGTTCTTCTTGCATGTGGCCCGCGTTGCCGAGGGCACTGCTCGGCCTGT CTTAAGGTACAAGAAGAGGAACGTACACCGGGCGCAACGGCTCCCGTGACGAGCCGGACA 90 CGCCGCAGAGGGCGCATGTCCGGGTGCCTGGATATGGCGCGTACGGCGTGCCCTCCGGC GCGGGCGTCTCCCGCGTACAGGCCCACGGACCTATACCGCGCATGCCGCACGGGAGGCCG 130 150 GTTAACCCCGAGGTTGGCCACGATGCCCCGGCCATCAGGTCTGGAATGCTAGCGTTCCAG CAATTGGGGCTCCAACCGTGCTACGGGGCCGGTAGTCCAGACCTTACGATCGCAAGGTC 190 **ACGAAGGTAACCCACAGTGACTCACACCACAAGTACTAGAATGCAAGCTGTTGCGGTGAG** TGCTTCCATTGGGTGTCACTGAGTGTGGTGTTCATGATCTTACGTTCGACAACGCCACTC 250 270 290 CGCCGCGCATAAGGGGGAGCCATGTCCGGGACGCGGAAAGCCTGACTCGATGACC **GCGGCGCGTATTCCCCCTCGGTACAGGCCCTGCGGCTGCCTTTCGGACTGAGCTACTGG** 310 330 350 ACCACCGACACCGGCCCAAGCCGGGCAGTGAGGCCGCCCTGCTCGCCAATGTCCGC T T D T G P K P G S E A A A L L A N V R 370 390 ACCTCGGGGCGCGGCTGTCCTCCGCGTTGTACGACATTCTGAAGAACCGGCTGCTCGAA TGGAGCCCCGCGCGACAGGAGGCGCAACATGCTGTAAGACTTCTTGGCCGACGAGCTT T S G A R L S S A L Y D I L K N R L L E 430 450 470 GGGCGCTATGCGGCAGGCGAGAAGATCGTCGTCGAGTCGATCCGGCAAGAGTTCGGGGTG CCCGCGATACGCCGTCCGCTCTTCTAGCAGCAGCTCAGCTAGGCCGTTCTCAAGCCCCAC G R Y A A G E K I V V E S I R Q E F G V 490 510 530 AGCAAGCAGCCGTCATGGACGCTCTGCGCCGCCTGTCCAGCGACAAGCTGGTCCACATC TCGTTCGTCGGCAGTACCTGCGAGACGCGGCGGACAGGTCGCTGTTCGACCAGGTGTAG S K Q P V M D A L R R L S S D K L V H I 570 590 550 GTTCCCCAGGTCGGTTGCGAGGTCGTCTCCTACGCCCCGCGCGAAGTGGAAGACTTCTAC CAAGGGGTCCAGCCAACGCTCCAGCAGAGGATGCGGGGCGCGCTTCACCTTCTGAAGATG V P Q V G C E V V S Y A P R E V E D F Y 630 650 610 ACCCTGTTCGGCGGTTTCGAAGGGACCATCGCCGCGGTAGCGGCCTCCCGGCGGACCGAG TGGGACAAGCCGCCAAAGCTTCCCTGGTAGCGGCGCCATCGCCGGAGGGCCGCCTGGCTC TLFGGFEGTIAAVAASRRTE 690 670 GCCCAGTTGCTGGACCTGACCTGATCTCGGCGCGGGTCGACGCCCTGATCACCTCCCAC CGGGTCAACGACCTCGACTGGACTAGAGCCGCCCAGCTGCGGGACTAGTGGAGGGTG A Q L L E L D L I S A R V D A L I T S H 730 750 GACCCGGTGGTCCGCGCCCCGCGGTACCGCGTGCACAACCGGGAGTTCCATGCGGCCATC CTGGGCCACCAGGCGCGCGCCCATGGCGCACGTGTTGGCCCTCAAGGTACGCCGGTAG D P V V R A R G Y R V H N R E F H A A I 790 810 830 H A M A H S R I M E E T S Q R M W D L S 850 870 890 GACTTCTTGATCAACACCACCGGCATCACCAACCCGCTCTCGAGCGCACTGCCCGACCGG CTGAAGAACTAGTTGTGGTGGCCGTAGTGGTTGGGCGAGAGCTCGCGTGACGGCCTGGCC D F L I N T T G I T N P L S S A L P D R 930 950 910 GTCGTACTGGTGGTGCTTTAGTGGCTCCGGTAGGCGTTGGCACTGCGTCGACGGCGGCG O H D H H E I T E A I R N R D A A A R 970 990 1010 GAGGCCATGGAACGCCACATCGTCGGCACCATCGCAGTAATCCGCGACGAATCCAACGCC CTCCGGTACCTTGCGGTGTAGCAGCCGTGGTAGCGTCATTAGGCGCTGCTTAGGTTGCGG EAMERHIVGTIAVIRDESNA 1050 1070 1030 CAGCTGCCGAGCTAGACCCCGATACCCGGGCCATCGACCGGCTCCGCTATCGCGCCACCT GTCGACGGCTCGATCTGGGGCTATGGGCCCGGTAGCTGGCCGAGGCGATAGCGCGGTGGA QLPS \* 1090 ACGCCGAGGGGGGACTCTCGGCCGTAGCGCTGCAGACGATCCACCGGCACCCTCCACGCT TGCGGCTCCCCCTGAGAGCCGGCATCGCGACGTCTGCTAGGTGGCCGTGGGAGGTGCGA 1150 1170 1190 GACCCCTGTCTCGCCCTAGAGGGCCGGCGCGCCGTCGATCACCTTTACCCTCATCCAGAG CTGGGGACAGAGCGGGATCTCCCGGCCGCGCGGCAGCTAGTGGAAATGGGAGTAGGTCTC 1250 1230 1210 ACTTGCGTCACCCTCTATGCCCGAGTAGCGTCTGAACTAGACGTCTAGCATTCTAGTTGA TGAACGCAGTGGGAGATACGGGCTCATCGCAGACTTGATCTGCAGATCGTAAGATCAACT 1270 1290 1310 GTGCTCCCTCTCGAAGATTCTCCAGAGAACCCCTCTCGAACATCCCCAGAAGAAAGGAGC

CACGAGGGAGAGCTTCTAAGAGGTCTCTTGGGGAGAGCTTGTAGGGGTCTTCTTTCCTCG 1330 1350 GGCCATGACGACCGCTTCGCACGCATCGTCCTTCGGGGCACGAGCCCACTTCCGCCCACA CCGGTACTGCTGCGAAGCGTGCGTAGCAGGAAGCCCCGTGCTCGGGTGAAGGCGGGTGT 1410 GATCGGGGAAGCCCGACCGTGAGCACCACACCTACCTCCCCGACGAAGACCTCACCGCTG CTAGCCCCTTCGGGCTGGCACTCGTGGTGTGGATGGAGGGGCTGCTTCTGGAGTGGCGAC 1470 CGGGTAGCGATGGCCAGCTTCATCGGTACCACCGTCGAGTACTACGACTTCTTCATCTAC GCCCATCGCTACCGGTCGAAGTAGCCATGGTGGCAGCTCATGATGCTGAAGAAGTAGATG M A S F I G T T V E Y Y D F F I Y 1510 1530 GGCACCGCGCCGCCGCTGTATTCCCTGAGTTGTTCTTCCCGGATGTCTCGTCCGCGATC CCGTGGCGCCGCGCGACCATAAGGGACTCAACAAGAAGGGCCTACAGAGAGCAGCGCTAG G T A A A L V F P E L F F P D V S S A I 1570 1590 . GILLSFATFSVGFLARPLGG 1630 1650 ATAGTGTTCGGGCACTTCGGTGACCGGGTCGGCCGCAAGCAGATGCTGGTGATCTCCCTG TATCACAAGCCCGTGAAGCCACTGGCCCAGCCGGCGTTCGTCTACGACCACTAGAGGGAC I V F G H F G D R V G R K Q M L V I S L 1730 1690 1710 GTCGGAATGGGCTCGGCCACCGTACTGATGGGATTGTTGCCCGGTTACGCCCAAATCGGG CAGCCTTACCCGAGCCGGTGGCATGACTACCCTAACAACGGGCCAATGCGGGTTTAGCCC V G M G S A T V L M G L L P G Y A Q I G 1790 1750 1770 ATCGCCGCCCCATCCTGCTGACCCTGCTGCGCCTGGTGCAGGGCTTTGCCGTCGGCGGC TAGCGGCGGGGTAGGACGACTGGGACGACGCGGACCACGTCCCGAAACGGCAGCCGCCG I A A P I L L T L L R L V Q G F A V G G 1850 1830 1810 GAGTGGGGTGGAGCCACCCTGATGGCCGTCGAGCACGCCCCCACCGCGAAGAAGGGCTTT CTCACCCCACCTCGGTGGGACTACCGGCAGCTCGTGCGGGGGTGGCGCTTCTTCCCGAAA EWGGATLMAVEHAPTAKKGF 1890 1870 TTCGGATCCTTCTCCCAGATGGGGGCACCCGCCGGGACCAGCGTCGCAACCCTGGCGTTC AAGCCTAGGAAGAGGGTCTACCCCCGTGGGCGGCCCTGGTCGCAGCGTTGGGACCGCAAG F G S F S Q M G A P A G T S V A T L A F

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AGAACTTIN	L L L L L L L L L L L L L L L L L L L	rgcg ACGC R 361 GCGA E 367 E GCGA H	CGCGA  O  AGCC P  O  ACCT TGGA L	GGA CCT D	GGC R TGT ACA V	TGG P CTC GAC S CCGA	CAC W CGA GGCT D	GGA CCT D 3 ACGA CGCT D 3	CCA CGT Q 1630 ACGT V 3690 ACAC	CAC W TGT AC! V	CTA I CCI AGGA L CCAC	GCGA	AGAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAC W AGAT TCTA I	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGAAGTT	L D CCC CCC L L ACCC	rgta M rcg1 Agc2 V	. CCG A . CCGG ACCC G
AGAACTTIN	L L L L L L L L L L L L L L L L L L L	rgcg ACGC R 361 GCGA CGCI E 367 CGCA	CGCGA  O  AGCC P  O  ACCT TGGA L	GGA CCT D	GGC R TGT ACA V	TGG P CTC GAC S CCGA	CAC W CGA GGCT D	GGA CCT D 3 ACGA CGCT D 3	CCA CGT Q 1630 ACGT CGCA V	CAC W TGT AC! V	CTA I CCI AGGA L CCAC	GCGA	AGAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAC W AGAT TCTA I	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GAP F SSO T T 710	L D CCC CCC L L ACCC	rgta M rcg1 Agc2 V	. CCG A . CCGG ACCC G
GAACTTI	CGA L ACG G G ACC TGG	TGCGACGC R 361 GCGACGCT E 367 CGCACGCT H 373	CGCCGCGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGGAACCGAACCGGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCGAACCAACCGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACAACA	CTA I GGA CCT D	GGC R TGT PACA V	TGG P CCTC S S CCGA AGCT E	CAC W CCGA GCT D AGAT	ACGA D ACGA CGCI D D CGCI D	CCA CGGTT Q 1630 ACGT CGCA V V 1690 CGTC S	CAC W TG1 AC# V	I CTA I CCTA AGGA L GGTC CCAC	GCG A CCG# ECTT EGGA/ F	GCCC G .AAC.I .TTGT Q	GAC W AGAT PCTA I GGTA CCAT	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GGAAGTY	ACCO	M TCG1 AGC2 V GGGC2 Q	. CCG A . CCGG AGCC G . AGTG PCAC W
GAACTTI	L CGA CGG CGG CGG CGG P	TGCGACGCACGCGCTACGCGCTACGCGCTACGCGCTACGCGCTACGCGCGCG	CGCCGCGAACTAACTAACTAACAACTAACAACAACAACAAACA	CTA I GGA CCT D	GGC R TGT PACA V V ACGT V	TGG P CCTC GAG S CCGA	CAC W CCGA CCGA GCT D AGAT I	ACGA ACGA ACGA D ACGA D CCGO V	CCA CCGTT Q 0 1630 CGGTA CGCA V V 1690 CGTCA S 3750	CAC W TGT ACI V CGAC CCTC	I POCTA	GCGAACTT	GCCC G .AC.; .TTGT Q .CTCTC W	GACGO	GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	GCTTCGAP F S50 . GGACCTCTT 710 . TCAAGTT	ACCO	M  FCGTA  M  FCGTA  FCG	. CCG A . CCGG AGCC G . AGTG PCAC W .
GAACTTI	L CGA CGG CGG CGG CGG P	TGCGACGCAR  361  361  EGCGACGCTAR  367  GGCACGCAR  AGCACACCACACACACACACACACACACACACACACAC	CGCCGCGAACTAACTAACTAACTAACTAACTAACTAACTA	CTA I GGA CCI D	GGC R TGT PACA V V ACGT V	TGG P CCTC GAG S CCGA E	CAC W CCGA CGGCT D AGAT I	GGGA GCCT  D  3 ACGA-GCCT D  CCGCT CCGCT CCGCT AGCA-GCCA CCGCT CCG	CCA CGGTT Q 1630 ACGT CGCA V V 1690 S S S S S S TGTO	CAC W TGT ACA CGAC CCTC R	I POCTA  I POCTA  L POCTA  L POCTA  E P	GCGAAGCTT	GCCG	AGAC AGAT AGAT CCTA I GGGTA Y	GGGGGCCCCGGCGCCGGCCGGCCGGCGCGGCGGCGGCGG	GCTTTGASTGASTGASTGASTGASTGASTGASTGASTGASTG	ACCO	M  FCGTA  M  FCGTA  FCG	. CCG A . CCGG AGCC G . AGTG PCAC W . ATCC FAGG
GAACTTI	L L L L L L L L L L L L L L L L L L L	TGCGACGCAR  361  361  EGCGACGCTAR  367  GGCACGCAR  AGCACACCACACACACACACACACACACACACACACAC	CGCCGCGAACTAACTAACTAACAACTAACAACAACAACAAACA	CTA I GGA CCI D	GGC R TGT PACA V ACGT V	TGG P CCTC GAG S CCGA E	CAC W CCGA CGGCT D AGAT I	GGGA GCCT  D  3 ACGA-GCCT D  CCGCT CCGCT CCGCT AGCA-GCCA CCGCT CCG	CCA CCGTT Q 0 1630 CGGTA CGCA V V 1690 CGTCA S 3750	CAC W TGT ACA CGAC CCTC R	I POCTA  I POCTA  L POCTA  L POCTA  E P	GCGAAGCTT	GCCG	AGAC AGAT AGAT CCTA I GGGTA Y	GGGGGCCCCGGCGCCGGCCGGCCGGCGCGGCGGCGGCGG	GCTTTGASTGASTGASTGASTGASTGASTGASTGASTGASTG	ACCO	M  FCGTA  M  FCGTA  FCG	. CCG A . CCGG AGCC G . AGTG PCAC W . ATCC FAGG
GAACTTIN N	L L L L L L L L L L L L L L L L L L L	TGCGACGCAR  361  GCGACGCT E  367  GCGACGCT H  AGCACGCT H  AGCACGCT H	ACCTA ACTA Y	CTA I GGA CCI D	GGC R TGT PACA V V ACGT V	TGG P CCTC GAG S CCGA E	CAC W CCGA CGGCT D AGAT I	GGGA GCCT D 3 ACGA CGCT D CCGT V V	CCA CGGT Q 1630 ACGT CGCA V 16690 S 3750 S TGTT ACAG	CAC W TGT AC CGAC CCTC R CCTC	I POCTA  I POCTA  L POCTA  L POCTA  E P	GCGAAGCTT	GCCG	AGAC AGAT AGAT CCTA I GGGTA Y	GGGGGCGCGCC	GCTTI GGAA F S50 GCCTC T T10 CCAAGTT N TGCAAGTT H	ACCO	M  FCGTA  M  FCGTA  FCG	. CCG A . CCGG AGCC G . AGTG PCAC W . ATCC FAGG
GAACTTIN N	L L L L L L L L L L L L L L L L L L L	TGCGACGCAR  361  361  EGCGACGCTAR  367  GGCACGCAR  AGCACACCACACACACACACACACACACACACACACAC	ACCTA ACTA Y	CTA I GGA CCI D	GGC R TGT PACA V V ACGT V	TGG P CCTC GAG S CCGA E	CAC W CCGA CGGCT D AGAT I	GGGA GCCT D 3 ACGA CGCT D CCGT V V	CCA CGGTT Q 1630 ACGT CGCA V V 1690 S S S S S S TGTO	CAC W TGT AC CGAC CCTC R CCTC	I POCTA  I POCTA  L POCTA  L POCTA  E P	GCGAAGCTT	GCCG	AGAC AGAT AGAT CCTA I GGGTA Y	GGGGGCGCGCC	GCTTTGASTGASTGASTGASTGASTGASTGASTGASTGASTG	ACCO	M  FCGTA  M  FCGTA  FCG	. CCG A . CCGG AGCC G . AGTG PCAC W . ATCC FAGG
GAACTI N CGAACTI N CGAACTI N	L ACGO G G ACCC PC CTG P E CTG G ACCC E G G ACCC P P CTG G G ACCC P P CTG G G ACC E G G A ACC E G G G G G G G G G G G G G G G G G G	TGCGACGCAR  361  GCGCACGCAR  367  CGCCACGCAR  AGCACACGCAR  AGCACACGCAR  H  379	CGCCCAACCTAACCTAACCTAACCTAACCTAACCTAACC	GGA CCT D	GGC R TGT PACA V AGTO S	TGG P CCTC GGAG S AGCT E	CCAC W CCGA GCT D AGAT TCTA I	GGGA GCGT D 3 ACGATCH D CGCT D CGCT V CGCT V V	CCA CGGTT Q 1630 ACGT CGCA V 16690 CGTC S 33750 F	CAC W TG1 ACA V CGAC CCTC AGAC C	CTA I CCCI AGGA L CCAC S	GCGAAGCGCGCGCGCGGCGGCGGCGCGCGCGCGCGCGCG	. ACA. ACA. ACA. ACA. ACA. ACA. ACA. AC	AGAT AGAT TCTA I GGTA Y ACGO	GGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGCGGCG	GCTTI GGAA F S50 GCCTC T T710 GCAAGTT N N 1770 H 830	ACCOTTEGE R	M  Property of the control of the co	ACCG A CCGG ACCC G AGTG P ATCC TAGG P
GAACTIN N	L CGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	reces R 361 BCGA CGCA E 367 CGCA H 373 AGCA H 379	CGCCCAACCTAACCTAACCTAACCTAACCTAACCTAACC	GGA CCTA D CGGA CCT D	GGC R TGT PACA V AGTC PCAC S	TGG P CCTC GAG S CCGG GGCC GGCC GGCC GGCC GGCC GG	CCAC W CCGA CCGA AGAN TCTA I	GGGA GCCT D ACGA CCGT V CCGT V	CGTO	CAC W TG1 AC2 CGAC CGCTC R CCTC AGAC C	I POCTA  GEORGE  GEORG  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE	GCGAAGGAAGGAAGGAAAGGAAAGGAAAGGAAAGGAAA	CTCTCAGACAW	GGAC W AGAT ICTA I GGTA Y ACGC A	GGGGGCCCCCRR 377 ACGTCCCCCRC V 31 CGGCCCCCCVV TCA	GCTTI GGAA F S50 GCCTC T 710 GCAAGT N N 1770 H 830	ACCOTTGGG	M  CGTA  M  CGTA  M  CGTA  CGGTA  CGGCA  CGG	CCG A CCGG ACCC G AGTG CCAC W ATCC IAGG P
GAACTIN N	L CGACCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	reces R 361 BCGA CGCA E 367 CGCA H 373 AGCA H 379	CGCCCAACTAACTAACTAACTAACTAACTAACTAACTAAC	GGA CCTA D CGGA CCT D	GGC R TGT PACA V AGT(CAC S	TGG P CCTC GAG S CCGG GGCC GGCC GGCC GGCC GGCC	CCAC W CCGA GCT D AGAT I CCGA GCT	GGGA GCCT D ACGA CCGCT V SAGCA V V	CGTOGCAC	CAC W TGT AC V CGAC CCTC CCCA GGT	I POCTA  GEORGE  GEORG  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE  GEORGE	GCGAAGGATCC	CCTCAGACAW  GCGCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GGAC W AGAT ICTA I GGTA Y ACGC A CGTT GCCA	GGGGGCCCCC V 31 TCAL	GCTTICGAAGTTOAAGCTTGG	ACCOTTGGG	M  CGTA  M  CGTA  M  CGTA  CGGTA  CGGCA  CGG	CCG A CGG AGCC G AGTG CAC W ATCC FAGG P AGGAA CCTT

3850 3870 3890 GATCGCGTTCGTCGAAGGGGTATGCAGGACCGGGTCTGCTCGAGTCCTACTCTCCTGA CTAGCGCAAGCAGCACTTCCCCATACGTCCTGGCCCAGACGAGCTCAGGATGAGAGGACT I A F V V K G Y A G P G L L E S Y S P E 3910 3930 3950 GCGTGTTCCGGTCGCCAACAGATCGTCGCTCGCCCAACCAGTCCCGCAAGGACTACGC CGCACAAGGCCAGCCGTTTGTCTAGCAGCGAGCGCGGTTGGTCAGGGCGTTCCTGATGCG R V P V G K Q I V A R A N O S R K D Y A 3970 3990 4010 CGGGCTGCGCGAATGGTTCGATCACGAGAGCGACCCGGTCGCCGGCCTGGCAAA GCCCGACGCGTTACCAAGCTAGTGCTCTCGCTGCTGGGCCAGCGGCGGCCGGACCGTTT G L R E W F D H E S D D P V A A G L A K 4050 4030 4070 GTTGAAGGAACCCTCGTCCGAAGGTGTTGCTCTGCGTGAGCGGCTGTACGAGGCGCTGGA CAACTTCCTTGGGAGCAGGCTTCCACAACGAGACGCACTCGCCGACATGCTCCGCGACCT LKEPSSEGVALRERLYEALE 4090 4110 4130 GGTGAAGAACGCCGAATTCAACGCCCAGGGCGTCGAACTCAACCAGCGCTACACCTCGTC CCACTTCTTGCGGCTTAAGTTGCGGGTCCCGCAGCTTGAGTTGGTCGCGATGTGGAGCAG V K N A E F N A Q G V E L N Q R Y T S S CGCGGTCGTTCCCGACCCCGAGGCGGCGAGGAAGTGTGGGTGCGCGATCGTGAGCTGTA GCGCCAGCAAGGGCTGGGGCTCCGCCCGCTCCTTCACACCCACGCGCTAGCACTCGACAT A V V P D P E A G E E V W V R D R E L Y 4210 4230 CCTGCAGGCCACCACCGGCCGGGCGCGAAGCTGCCGCATGCGTGGCTGGTCGGCGCCGA GGACGTCCGGTGGTGGGCCGCCCCGCGCTTCGACGCGTACGCACCGACCAGCCGCGCT LOATTRPGAKLPHAWLVGAD 4270 4290 4310 CGGAACCCGCATCTCCACCCTCGACGTCACCGGCAAGGGAATGATGACCCTGCTGACCGG GCCTTGGGCGTAGAGGTGGAGCTGCAGTGGCCGTTCCCTTACTACTGGGACGACTGGCC G T R I S T L D V T G K G M M T L L T G 4370 4330 4350 ACTCGCCGCCAGCATGGAAGCGTGCCGCCCAAACTCGACCTGCCGTTCCTGCGGAC TGAGCCGCCGGTCCGTACCTTCGCACGGCGGCGGTTTGAGCTGGACGGCAAGGACGCCTG L G G Q A W K R A A A K L D L P F L R T 4430 4390 4410 CGTCGTTGTCGGCGAACCCGGCACCATCGACCCTTACGGATACTGGCGGCGGGTCCGCGA GCAGCAACAGCCGCTTGGGCCGTGGTAGCTGGGAATGCCTATGACCGCCGCCCAGGCGCT V V V G E P G T I D P Y G Y W R R V R D

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4490

4470

CATCGACGAGGCCGGCCCTGCTCGTGCGGCCCGACGGCTACGTCGCGTGGCGACACAG

4450

GTAGCTGCTCCGGCCGCGGACGACGACGCCGGGCTGCCGATGCAGCGCACCGCTGTGTC I D E A G A L L V R P D G Y V A W R H S 4530 4550 TGCTCCGGTCTGGGACGACACCGAAGCGCTCACCAGCCTCGAGAACGCTCTCACCGCGGT ACGAGGCCAGACCCTGCTGTGGCTTCGCGAGTGGTCGGAGCTCTTGCGAGAGTGGCGCCA A P V W D D T E A L T S L E N A L T A V 4570 4590 4610 CCTCGACCACTCGGCCAGCGACAACGGGAACCCGAGCGGCACAAACGAGCCGCAGTACAG GGAGCTGGTGAGCCGGTCGTTGCCCTTGGGCTCGCCGTGTTTGCTCGGCGTCATGTC L D H S A S D N G N P S G T N E P Q Y S 4650 4670 4630 CACCGGGCCGTGCCGATCGTCGTTCCGCACGTTACCGCCGAGGATGCAGCACCAGCTTC GTGGGCCCGGCACGCTAGCAGCAAGGCGTGCAATGGCGGCTCCTACGTCGTGGTCGAAG TRAVPIVVPHVTAEDAAPAS 4710 4730 4690 CGCCACCGCACCACACAGTCGAGGGAGAGAACCGATGACCCGTCCTTACACCAGCGTC GCGGTGGCGTGTGTCAGCTCCCTCTCTTGGCTACTGGGCAGGAATGTGGTCGCAG ATRTTTVEGENR\* MTRPYTSV 4750 4770 4790 W D D L N Q V E F S Q G F I Q A G P Y R 4850 4810 4830 ACCCGATACCTGCACGCCGCGATTCGTCCAAGCCCACGCTGATCCTGCTGCACGCATC TGGGCTATGGACGTGCGGCCGCTAAGCAGGTTCGGGTGCGACTAGGACGACGTGCCGTAG TRYLHAGDSSKPTLILLHGI 4910 4870 4890 ACCGGCCACGCCGAGGCGTACGTGCGCAATCTGCGCTCGCATTCCGAGCACTTCAACGTC TGGCCGGTGCGGCTCCGCATGCACGCGTTAGACGCGAGCGTAAGGCTCGTGAAGTTGCAG T G H A E A Y V R N L R S H S E H F N V 4950 4970 4930 TGGGCAATCGACTTCATCGGCCACGGCTATTCGACCAAGCCCGACCACCCGCTCGAGATC ACCCGTTAGCTGAAGTAGCCGGTGCCGATAAGCTGGTTCGGGCTGGTGGGCGAGCTCTAG WAIDFIGHGYSTKPDHPLEI 5030 5010 4990 AAGCACTACATCGACCACGTGCTGCAGTTGCTGGACGCCATCGGCGTCGAGAAGGCCTCG TTCGTGATGTAGCTGGTGCACGACGTCAACGACCTGCGGTAGCCGCAGCTCTTCCGGAGC K H Y I D H V L Q L L D A I G V E K A S 5090 5070 5050 TTTTCCGGGGAGTCTCTCGGCGGTTGGGTCACCGCCCAGTTCGCGCACGACCATCCCGAG AAAAGGCCCCTCAGAGAGCCGCCAACCCAGTGGCGGGTCAAGCGCGTGCTGGTAGGGCTC F S G E S L G G W V T A Q F A H D H P E

10/16

5130

5150

AAGGTCGACCGGATCGTGCTCAACACCATGGGCGGCACCATGGCCAACCCTCAGGTGATG TTCCAGCTGGCCTAGCACGAGTTGTGGTACCCGCCGTGGTACCGGTTGGGAGTCCACTAC K V D R I V L N T M G G T M A N P Q V M

5190

GAACGTCTCTATACCCTGTCGATGGAAGCGGCGAAGGACCCGAGCTGGGAACGCGTCAAA CTTGCAGAGATATGGGACAGCTACCTTCGCCGCTTCCTGGGCTCGACCCTTGCGCAGTTT E R L Y T L S M E A A K D P S W E R V K

5230

5250

5270

GCACGCCTCGAATGGCTCATGGCCGACCCGACCATGGTCACCGACGACCTGATCCGCACC CGTGCGGAGCTTACCGAGTACCGGCTGGGCTGGTACCAGTGGCTGCTGGACTAGGCGTGG ARLEWLMADPTMVTDDLIRT

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CGCCAGGCCATCTTCCAGCAGCCGGATTGGCTCAAGGCCTGCGAGATGAACATGGCACTG GCGGTCCGGTAGAAGGTCGTCGGCCTAACCGAGTTCCGGACGCTCTACTTGTACCGTGAC RQAIFQQPDWLKACEMNMAL

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CAGGACCTCGAAACCCGCAAGCGGAACATGATCACCGACGCCACTCTCAACGGCATCACG GTCCTGGAGCTTTGGGCGTTCGCCTTGTACTAGTGGCTGCGGTGAGAGTTGCCGTAGTGC Q D L E T R K R N M I T D A T L N G I T

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CGCATCGCCTCCCACATCCCGGGCGCCAAGCTGGCCATCATGGAGAACTGTGGCCACTGG GCGTAGCGGAGGGTGTAGGGCCCGCGGTTCGACCGGTAGTACCTCTTGACACCGGTGACC RIASHIPGAKLAIMENCGHW

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CCCCAGTACGAGGACCCCGAGACCTTCAACAAGCTGCATCTGGACTTCCTCCTCGGTCGC GGGGTCATGCTCCTGGGGCTCTGGAAGTTGTTCGACGTAGACCTGAAGGAGGAGCCAGCG PQYEDPETFNKLHLDFLLGR

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TCTCACTTACCCGACCTATTGCGCTCTCGTCCGGACCCCCGGAGAGAAAGCGCCGAAGCA AGAGTGAATGGGCTGGATAACGCGAGAGCAGGCCTGGGGGCCTCTCTTTCGCGGCTTCGT

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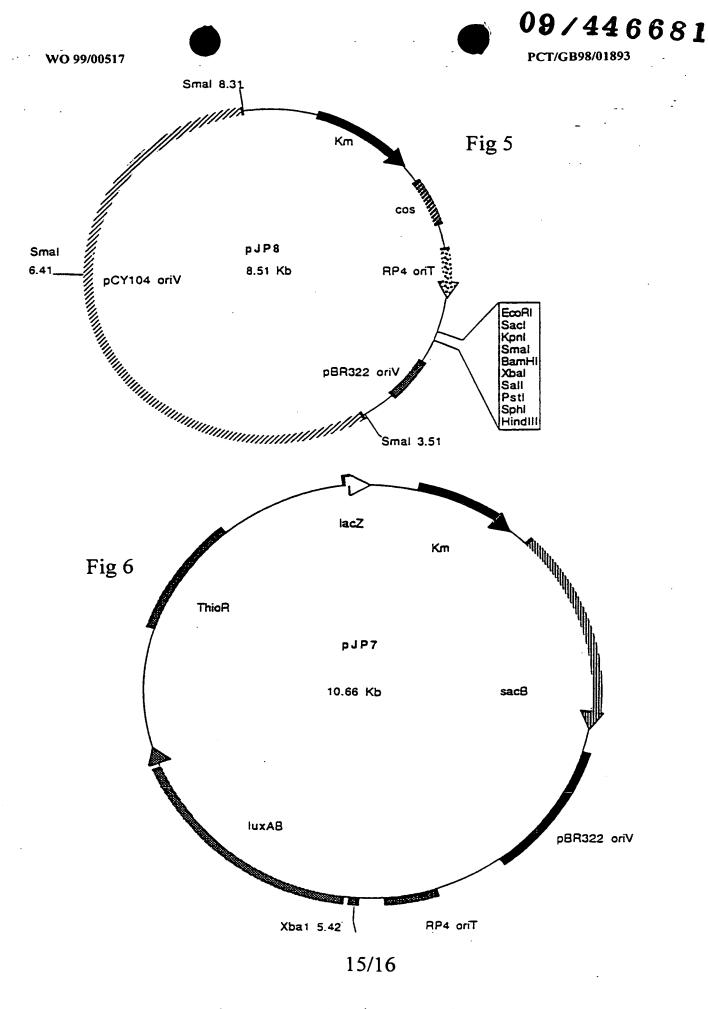
GCAGCAAGGAGACCGCCGCGATGCCTGTAGCGCTGTGCGCGATGTCGCACTCCCCCTGA

11/16

CGTCG	TTCC'	TCTG	GCG	GCGC	TAC M	CGG. P	ACA:	rcgo A	CGA(	CAC	GCG(	CTA M	CAG S	CGT(	GAG( S	GGG(	GGA L	CT M
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CCGG	CGGC	CTGT	CCC	ACG/	ACC	CGC	CGGʻ	TCC	CGC	AGT"	rcg	CCA	CCG	CGC	CAG	AGG	AAG'	TGC
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6370 6390 6410 CGCAGTAGTGGCGGCCCTGAAGCGGCGGCGTGGCGGCGGTAGGTCGGTGACTTGG V I T A G R D F A A G T A A I Q P L N P 6470 6430 6450 CCGAATGGGACCGCACCTCCTCGACGTCCTCGCCTCCGGCGACCTCGAGCAGATCGACG GGCTTACCCTGGCCGTGGACGAGCTGCAGGAGCGGAGGCCGCTGGAGCTCGTCTAGCTGC E W D R H L L D V L A S G D L E Q I D A 6490 6510 6530 CGTGGACCAACGACTGGTTCGTCGAACAGGCCGGACACTCCTCCCACGAAGTGCGCACCT GCACCTGGTTGCTGACCAAGCAGCTTGTCCGGCCTGTGAGGAGGGTGCTTCACGCGTGGA W T N D W F V E Q A G H S S H E V R T W 6570 6590 6550 GGATCGCCGCGTACGCGGCAATGAGCGCCGCCGGGAAGTACCGCGTCACCTCGACCTTCT CCTAGCGGCGCATGCGCCGTTACTCGCGGCGCCCTTCATGGCGCAGTGGAGCTGGAAGA T A A Y A A M S A A G K Y R V T S T F Y 6630 6610 ACCGCGAAATCCACGAGTGGATAGCAGGATTCGGGATTACTACCGCCGTCGCCGTCGACG TGGCGCTTTAGGTGCTCACCTATCGTCCTAAGCCCTAATGATGGCGGCAGCGGCAGCTGC REIHEWIAGFGITTAVAVDE 6690 6710 6670 AATAGACCCCGCCGCTCCCGCCCCGCAGTCCCAACGAAGGGTGGCCCCGGATGACCTCCG TTATCTGGGGCGGGGGGGGGGGGCGTCAGGGTTGCTTCCCACCGGGGCCTACTGGAGGC MTSV 6770 6730 6750 TCCGCCCGTGCTCGCCGTCGAACGCGGGCTGGTCGGTGGGCAGGAAGACCTCATCGC AGGCGGGCACGAGCGGCAGCCACTTGCGCCCGACCAGCCACCCGTCCTTCTGGAGTAGCG R P C S P S V N A G W S V G R K T S S P 6830 6790 6810 CGACATCGCCCTCGACCTCGCAGCTCGTCAGTAGGAATGCGCACGGGCCGACGAGTCGCG GCTGTAGCGGGAGCTGGAGCGTCGAGCAGTCATCCTTACGCGTGCCCGGCTGCTCAGCGC T S P S T S Q L V S R N A H G P T S R A 6870 6890 6850 CTGGTCACCGGGGCCAGCCGCGCATCGGGGCGCCATCGCAGATGCGGTGGCCGCCTCC GACCAGTGGCCCCGGTCGGCGCCGTAGCCCCGCCGGTAGCGTCTACGCCACCGGCGGAGG G H R G Q P R H R G G H R R C G G R L R 6950 6930 6910 GGTGCCGCCGTAATCGTCCACTACGGATCCGATCGGACGCCGCCGCTGCGGTGTCGACG CCACGGCGGCATTAGCAGGTGATGCCTAGGCTAGCCTGCCGGCGGCGACGCCACAGCTGC CRRNRPLRIRSDGRRCGVDG 7010 6970 6990 GCATCACGGCTGCCGGGGCCTCGCGGCTGCGGTCCAGGCCGACCTGTCCCGACCCGAGG

CGTA										CCA	GGT	CCG	GCT	GGA	CAG	GC'	rgg	GCT	CC
I	T	Α	A	G	G	L	A	A	Α	V	Q	A	D	L	S	R	P	E	G
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GGCC'																			
CCGG																			_
P	E	E	L	M	R	E	F	D	S	A	L	D	G	L	G	L	D	R	G
	70	090						71:	10						713	0			
		•				•			•			•				•			•
GGCT	CGA	CATO	CTY	CGT	CAA	CAA	CGC	CGG	AAT	CAG	TCG	GCG	CGG.	AGC	GCT	CGA	GCG	CGT	CA
CCGA	GCT	STAC	3GA(	GCA	GTT	GTT	GCG	GCC:	rta(	GTC.	AGC	CGC	GCC'	TCG	CGA	GCT	CGC	GCA	GT
L	D	I	L	V	N	N	Α	G	I	S	R	R	G	Α	L	E	R	V	${f T}$
	7:	150						71	70						719	0			
CTGT	CGA	GGA'	rtt(	CGA	CCG'	TCT	GGT	CGC	ACT	CAA	CCA	GCG	CGC	ccc	GTT	CTT	CGT	GAC	TC
GACA																			
v	E	D	F	D	R	L	V		L	N	0	R	A	P	F	F	v	T	R
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	7:	210						72	30						725	0			
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CCGT																			
Н	A	L	P	R	M	Н	D	G	G	R	I	V	N	I	S	S	G	s	Α
٠	7	270						72	90						731	0	•		
CCCG	CTA	CGC	CAG	ACC	CGA	CGT	CAT	CAG	CTA	CGC	CAT	GAC	CAA	GGG	GGC	GAT	CGA	GGT	GC
GGGC																			
R	Y	A	R	P	D	v	I	S	Y	A	M	T	K	G	A	I	E	v	L
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TCAC																			
AGTG													_		_				
${f T}$	R	A	L	Α	V	D	V	G	E	R	G	I	T	Α	N	Α	V	Α	P
	7	390						74	10						743	0			
CGGC	CGC	GCT	CGA	TAC	CGA	CAT	GAA	CGC	GCA	СТС	GCT	тсе	CGG	TGA	CGA	CCA	TGC	CCG	CA
GCCG																			
A	A	L	D	T	D	M	N	A	Н	W	L	R	G	D	D	н	A	R	T
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CCAC																			
GGTG	GCG	GCG	CAG	GTC	GTG	ACC	TG	CGC	TTT	TG	AGCC	GTC	GCC	CCI	CCI	GTA	GCG	GCC	CT
T	Α	Α	S	T	T	Α	L	R	K	L	Α	T	Α	E	D	I	Α	Α	I
	7	510				-		75	30						755	0			
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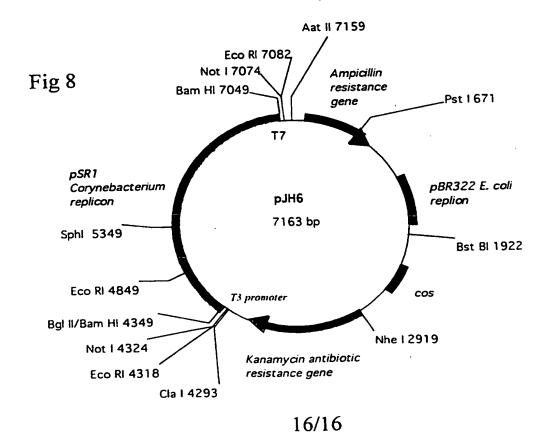


**SUBSTITUTE SHEET (RULE 26)** 



Bsu36 | 6514, Kanamycin Sca | 6463 cos resistance gene Sac II 6289 -Ava || 998 Bsa | 6117\_ BstB | 1163 Afl II 6025 pSR1 pRV1 RP4 Fig 7 Corynebacterium ori T 7205 bp replicon Esp ! 5199 PfIM I 4803 <-Plac pUC E. coli Eco RI 4745 replicon Pml I 4716 Pst I 3547 Ssp I 4205 Sal I 3553 Xba | 3559 TrpA Terminator BamH I 3565 3608

> Sma I 3570 Kpn I 3574



SUBSTITUTE SHEET (RULE 26)